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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/806,767	08/10/2001	Dieter Berger	0147-0223P	4759

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BIRCH STEWART KOLASCH & BIRCH
PO BOX 747
FALLS CHURCH, VA 22040-0747

EXAMINER	
BAUM, STUART F	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 04/08/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/806,767	BERGER ET AL.	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *09 January 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-32* is/are pending in the application.

4a) Of the above claim(s) *11-14,19 and 31* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-10,15-18 and 20-31* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *03 April 2001* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *4/3/01 & 2/12/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Claims 1-32 are pending.

Applicant's election with traverse of Group I, claims 1-10, 15-18 and 20-21, including SEQ ID NO:1 encoding SEQ ID NO:2, filed 1/9/2004, is acknowledged. The traversal is on the ground(s) that the International Preliminary Examination Authority did not find unity of invention lacking (page 12, 2nd paragraph of response). Applicants contend that the Jarai et al reference does not teach a nucleic acid that would modify stomata density when transformed into a plant

This is not found persuasive because the Examiner is not held to the examining or lack or unity practices of the European Searching Authority. Jarai et al teach a subtilisin-like protease, that inherently comprises domains of a subtilisin-like protease. Given the lack of any evidence to the contrary, a nucleic acid of Jarai et al, would function like a subtilisin-like protease when transformed into a plant and said plant would exhibit modified stomata density.

The requirement is still deemed proper and is therefore made FINAL.

Claims 22-32 have been newly added.

Claim 32 is withdrawn from consideration for being drawn to the invention of Group V.

Claims 11-14 and 19 are withdrawn from consideration for being drawn to non-elected inventions.

2. Claims 1-10, 15-18, and 20-31 are examined in the present office action.

Specification

3. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See for example page 35, 1st paragraph of Example 2; and page 36, line 3. See MPEP § 608.01.

Claim Objections

4. Claim 1 is objected to for reading on non-elected inventions. Correction is required.

In claims 7, and 26, line 2, "characteristics" is misspelled.

Claims 7 and 26 are objected to for omitting to specify that the recombinant DNA molecule is introduced "into a plant". For purposes of compact prosecution, the Office interprets this claim to mean that the recombinant DNA molecule is introduced into a plant. Correction is requested.

Written Description #1

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

5. Claims 1-10, 15-18, and 21-31 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to

reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to nucleic acid molecules encoding a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or a nucleic acid molecule that hybridizes therewith or that hybridizes with the complement of SEQ ID NO:1 or with the complement of the nucleic acid molecule encoding SEQ ID NO:2, or a nucleic acid molecule encoding a protein exhibiting 65% sequence identity to the protein encoded by SEQ ID NO:1, or a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or a nucleic acid molecule that hybridizes with any of the before mentioned nucleic acid sequences, or a nucleic acid molecule encoding any subtilisin-like serine protease, or encoding any biologically active fragment of any of the encoded polypeptides mentioned above, a recombinant DNA molecule and transgenic plant comprising said nucleic acid molecule, and methods comprising said nucleic acid sequence.

Applicants disclose SEQ ID NO:1 encoding the SDD1 protein of SEQ ID NO:2 (pages 35, last 4 lines and page 36, line 1; and sequence listing).

The Applicants do not identify essential regions of SDD1 protein encoded by SEQ ID NO:1, nor do Applicants describe any polynucleotide sequences that hybridize to a nucleic acid sequence encoding a D, H, or S domain of SEQ ID NO:2 or the substrate binding site of the protein of SEQ ID NO:2, or a protein exhibiting 65% sequence identity to the protein encoded by SEQ ID NO:1, or a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2 and that encode a functional SDD1 protein.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). Applicants fail to describe a representative number of polynucleotide sequences encoding a SDD1 protein falling within the scope of the claimed genus of polynucleotides which hybridize to a nucleic acid sequence encoding a D, H, or S domain of SEQ ID NO:2 or encoding the substrate binding site of the protein of SEQ ID NO:2, or encoding a protein exhibiting 65% sequence identity to the protein encoded by SEQ ID NO:1, or a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2. Applicants only describe a single cDNA sequence of SEQ ID NO:1. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of polynucleotides. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for the SDD1 protein, it remains unclear what features identify an Arabidopsis SDD1 protein. Since the genus

of SDD1 proteins has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Sequences that hybridize with SEQ ID NO:1 or encode a protein exhibiting 65% sequence identity with a protein comprising a D, H, or S domain of SEQ ID NO:2 or comprising the substrate binding site of the protein of SEQ ID NO:2 encompass naturally occurring allelic variants, mutants of SDD1 protein, as well as sequences encoding proteins having no known SDD1 activity, of which Applicant is not in possession. Absent of such disclosure, one skilled in the art cannot determine the genus of sequences based upon the disclosure of the sequence of SEQ ID NO:1 encoding SEQ ID NO:2 with any certainty or predictability. Accordingly, the specification fails to provide an adequate written description to support the hybridization language or percent identity language or domain language as set forth in the claims. (See Written Description guidelines published in Federal Register/Vol. 66, No.4/Friday, January 5, 2001/Notices: p.1099-1111).

Written Description #2

6. Claims 20 and 21 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to a method comprising a foreign nucleic acid molecule, the presence of which or the expression of which results in an increased activity of any subtilase or a

subtilisin-like serine protease or a nucleic acid molecule regulating the expression of any subtilisin-like serine protease.

Applicants disclose SEQ ID NO:1 encoding the SDD1 protein of SEQ ID NO:2 (pages 35, last 4 lines and page 36, line 1; and sequence listing).

Applicants do not identify essential regions of the genus of foreign nucleic acid molecules that have a function as claimed by Applicant, nor do Applicants describe any genus of foreign nucleic acid molecules, the presence of which or the expression of which results in an increased activity of any subtilase or any subtilisin-like serine protease, other than the single example of SEQ ID NO:1. The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). Applicants fail to describe a representative number of polynucleotide sequences whose presence or expression results in an increased activity of a subtilase. Applicants only describe a single nucleic acid sequence of SEQ ID NO:1.

Furthermore, Applicants fail to describe structural features common to members of the claimed genus of polynucleotides. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for the foreign nucleic acid molecule to affect expression of any subtiliase, it remains unclear what features identify any foreign nucleic acid molecules whose presence or expression results in an increased activity of any subtilase. Since the genus of foreign nucleic acid molecules has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Sequences whose presence or expression increase expression of any subtilase encompass a multitude of DNA molecules, examples of which are molecules encoding any subtilase protein, DNA molecules encoding transcription factors that increase expression of any subtilase protein, or DNA molecules encoding repressors of inhibitors of subtilase expression. Applicants are only in possession of SEQ ID NO:1. Applicants are not in possession of the multitude of other molecules. Absent of a disclosure to said molecules, one skilled in the art cannot determine the genus of sequences based upon the disclosure of the sequence of SEQ ID NO:1 with any certainty or predictability. Accordingly, the specification fails to provide an adequate written description to support the broad claim drawn to any foreign nucleic acid molecule, the presence of which or expression of which results in an increased activity of any subtilase. (See Written Description guidelines published in Federal Register/Vol. 66, No.4/Friday, January 5, 2001/Notices: p.1099-1111).

Scope of Enablement

7. Claims 1-10, 15-18, and 20-31 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a nucleic acid sequence comprising SEQ ID NO:1 operably linked to a promoter, and transformed into an Arabidopsis plant to produce leaves with a reduction in stomata density, does not reasonably provide enablement for claims drawn to nucleic acid molecules encoding a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or a nucleic acid molecule that hybridizes therewith or that hybridizes with the complement of SEQ ID NO:1 or with the complement of the nucleic acid molecule encoding SEQ ID NO:2, or a nucleic acid molecule encoding a protein exhibiting 65% sequence identity to the protein encoded by SEQ ID NO:1, or a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or a nucleic acid molecule that hybridizes with any of the before mentioned nucleic acid sequences, or a nucleic acid molecule encoding any subtilisin-like serine protease, or encoding any biologically active fragment of any of the encoded polypeptides mentioned above; or a nucleic acid molecule comprising a foreign nucleic acid molecule, the presence of which or the expression of which results in an increased activity of any subtilase or a subtilisin-like serine protease or a nucleic acid molecule regulating the expression of any subtilisin-like serine protease and plant transformation therewith, to yield any plant with altered stomata characteristics, lower conductance of stomata, decreased water consumption, decreased water loss, sustained photosynthesis under high intensity conditions, reduced leaf temperature, improved disease resistance, improved fresh and dry weight, enhanced sugar content, enhanced protein in plant leaves, or enhanced CO_2 uptake and H_2O release. The

specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

The claims are drawn to a nucleic acid molecules encoding a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or a nucleic acid molecule that hybridizes therewith or that hybridizes with the complement of SEQ ID NO:1 or with the complement of the nucleic acid molecule encoding SEQ ID NO:2, or a nucleic acid molecule encoding a protein exhibiting 65% sequence identity to the protein encoded by SEQ ID NO:1, or a protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or a nucleic acid molecule that hybridizes with any of the before mentioned nucleic acid sequences, or a nucleic acid molecule encoding any subtilisin-like serine protease, or encoding any biologically active fragment of any of the encoded polypeptides mentioned above, a recombinant DNA molecule and transgenic plant comprising said nucleic acid molecule, and methods as specified in claims

7, 20, 21, 26, and 31 comprising said nucleic acid sequences. Applicants also claim a method comprising a foreign nucleic acid molecule, the presence of which or the expression of which results in an increased activity of any subtilase or a subtilisin-like serine protease or a nucleic acid molecule regulating the expression of any subtilisin-like serine protease.

Applicants disclose the Arabidopsis mutant R-558, in which the density of stomata is increased. Applicants subsequently isolated SEQ ID NO:1, the wild-type gene whose mutant allele was responsible for the mutant phenotype (pages 34-36, Examples 1-2). Applicants provide guidance for transforming Arabidopsis with SEQ ID NO:1 to produce plants with a reduced stomata density (pages 36-39, Example 3 and pages 40-41, Example 5).

Applicants fail to teach any nucleic acid molecules encoding any protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or any nucleic acid molecule that hybridizes therewith or that hybridizes with the complement of SEQ ID NO:1 or with the complement of the nucleic acid molecule encoding SEQ ID NO:2, or any nucleic acid molecule encoding a protein exhibiting 65% sequence identity to the protein encoded by SEQ ID NO:1, or any protein comprising at least the D, H, or S region or the substrate binding site of the subtilisin-like serine protease of SEQ ID NO:2, or any nucleic acid molecule that hybridizes with any of the before mentioned nucleic acid sequences, or any nucleic acid molecule encoding any subtilisin-like serine protease, or encoding any biologically active fragment of any of the encoded polypeptides mentioned above, a recombinant DNA molecule and transgenic plant comprising said nucleic acid molecule, or methods as specified in claims 7, 20, 21, 26, and 31 comprising any of said nucleic acid sequences. Applicants also fail to teach a method comprising any foreign nucleic acid molecule, the presence of which or the

expression of which results in an increased activity of any subtilase or a subtilisin-like serine protease or any nucleic acid molecule regulating the expression of any subtilisin-like serine protease.

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids that either hybridize to a domain of SEQ ID NO:2 encoded by SEQ ID NO:2 or which nucleic acids that exhibit 65% of SEQ ID NO:2 will encode a protein with the same activity as a protein encoded by SEQ ID NO:1. The prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex, and the positions within the protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310, 1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino acid in a sequence. For example, the replacement of a glycine residue located within the START domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or aspartic acid residue, alters the sterol/lipid binding domain (McConnell et al, Nature 411 (6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

The state-of-the-art teaches that isolating DNA fragments using stringent hybridization conditions, does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe. Fourgoux-Nicol et al (1999, Plant Molecular Biology 40 :857-872) teach the isolation of a 674bp fragment using a 497bp probe incorporating stringent hybridization conditions comprising three consecutive 30 minute rinses in 2X, 1X and 0.1X SSC with 0.1% SDS at 65^0C (page 859, left column, 2nd paragraph). Fourgoux-Nicol et al also teach

that the probe and isolated DNA fragment exhibited a number of sequence differences comprising a 99bp insertion within the probe and a single nucleotide gap, while the DNA fragment contained 2 single nucleotide gaps and together the fragments contained 27 nucleotide mismatches. Taking into account the insertions, gaps and mismatches, the longest stretch of contiguous nucleotides to which the probe could hybridize consisted of 93bp of DNA (page 862, Figure 2).

Applicants' claims are drawn to methods of modifying the expression of any subtilase, comprising introducing into a plant any nucleic acid sequence that somehow effects the expression of a subtilase, or Applicant has claimed fragments of SEQ ID NO:1 or sequences that hybridize to a nucleic acid sequence encoding a protein with partial similarity to Applicants' SEQ ID NO:2, but Applicant has not provided guidance for selecting a nucleic acid sequence that will effect subtilase expression. Applicants have not disclosed how one makes or isolates any of the sequences that are encompassed by Applicants' broad claims. Applicants have not taught which regions of the respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences.

Applicants have claimed methods of altering the development or physiology of plants but Applicants have only disclosed that transforming a plant with SEQ ID NO:1 only decreases the stomata density. Applicants have not disclosed that this method also changes the water usage, photosynthetic capabilities or efficiencies, sugar or protein content, fresh or dry weight, or disease resistance of the transformed plants. Applicants have not shown that plants with decreased density of stomata actually lose less water than a wild-type plant. And if plants do

lose less water than a wild-type plant, how will this reduce the leaf temperature and not raise it? In addition, how will water release be enhanced, if water release is accomplished through stomata?

Applicants have not provided examples or guidance for selecting a sequence out of the multitude of sequences that are encompassed by Applicant's broad claim language, that gives the expected results when transformed into a plant. Transforming plants with heterologous genes that are involved in plant development produce unpredictable results. Kano-Murakami et al (1993, FEBS 334:365-368) teach introducing the *Oryza sativa* homeobox 1 (OSH1) gene into tobacco. OSH1 is a rice homologue of the *Knotted-1* homeobox gene from maize and would be encompassed by Applicant's broad claim language. Kano-Murakami et al teach transgenic tobacco plants comprising the OSH1 gene display a "range of phenotypes which include abnormalities in leaf and petal shape as well as stem height and number" (page 365, right column, 1st paragraph).

In the absence of guidance, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through the multitude of non-exemplified sequences, either by using non-disclosed fragments of SEQ ID NO:1 as probes or by designing primers to undisclosed regions of SEQ ID NO:1 and isolating or amplifying fragments, subcloning the fragments, producing expression vectors and transforming plants therewith, in order to identify those, if any, that when over-expressed, produce a plant with reduced density of stomata and are encompassed by Applicants' claims.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

Claim Rejections - 35 USC § 102

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

8. Claims 1-3, 18, 23-25 and 30 are rejected under 35 U.S.C. 102(b) as being anticipated by Vysotskaia et al et al (May, 1998, NCBI Accession Number AC002411).

The claims are drawn to a recombinant DNA molecule comprising a nucleic acid molecule of SEQ ID NO:1, wherein the nucleic acid molecule is derived from a plant, wherein a vector comprises the recombinant DNA molecule, and a host cell transformed therewith. The claims are also drawn to a kit comprising SEQ ID NO:1. The Office interprets the "kit" to comprise only the nucleic acid sequence of SEQ ID NO:1 because Applicants have not specified other items encompassed in the kit.

Vysotskaia et al teach a nucleic acid sequence exhibiting 100% sequence identity with SEQ ID NO:1. For purposes of molecular biology, the sequence of Vysotskaia et al would be in a vector and transformed into a host cell, and as such, Vysotskaia et al anticipate the claimed invention.

9. Claims drawn to a nucleic acid sequence comprising SEQ ID NO:1 encoding SEQ ID NO:2, operably linked to a promoter, and transformed into an Arabidopsis plant to produce leaves with a reduction in stomata density are free of the prior art given the failure of the prior

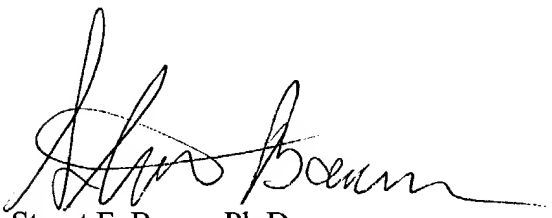
art to teach or reasonably suggest a plant transformed with SEQ ID NO:1 encoding SEQ ID NO:2.

10. No claims are allowed.

11. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.



Stuart F. Baum Ph.D.
Patent Examiner
Art Unit 1638
March 31, 2004